

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/582,973
Source: 1FWP
Date Processed by STIC: 6/26/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)**
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314**

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/582,973

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleic
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 Skipped Sequences
 (OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 Skipped Sequences
 (NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

11 Use of <220>
 48 Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/582,973

DATE: 06/26/2006
TIME: 13:30:45

Input Set : A:\sequence list.txt
Output Set: N:\CRF4\06262006\J582973.raw

2 <110> APPLICANT: Toshikazu Nakamura
W--> 3 <120> TITLE OF INVENTION: Glycosylation-deficient hepatocyte growth factor
W--> 4 <130> FILE REFERENCE: N13F1456
C--> 5 <140> CURRENT APPLICATION NUMBER: US/10/582,973
C--> 5 <141> CURRENT FILING DATE: 2006-06-15
W--> 5 <160> NUMBER OF SEQ ID: 8

ERRORED SEQUENCES

106 <210> SEQ ID NO: 2
107 <211> LENGTH: 723
108 <212> TYPE: PRT
109 <213> ORGANISM: Sapiens *see p. 3, line 100*
W--> 110 <220> FEATURE: Hepatocyte growth factor of five amino acids-deleted type *move this to 12237 line. 12207*
111 <223> OTHER INFORMATION: *never has*
W--> 112 <400> SEQUENCE: 2
113 Met Trp Val Thr Lys Leu Leu Pro Ala Leu Leu Gln His Val Leu
114 5 10 15
115 Leu His Leu Leu Leu Pro Ile Ala Ile Pro Tyr Ala Glu Gly Gln
116 20 25 30
117 Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys Thr
118 35 40 45
119 Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys Val
120 50 55 60
121 Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly Leu
122 65 70 75 80
123 Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln Cys
124 85 90 95
125 Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu Phe
126 100 105 110
127 Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn Cys
128 115 120 125
129 Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr Lys
130 130 135 140
131 Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu His
132 145 150 155 160
133 Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn Tyr Cys Arg Asn Pro Arg
134 165 170 175
135 Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr Ser Asn Pro Glu Val Arg
136 180 185 190
137 Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser Glu Val Glu Cys Met Thr
138 195 200 205

*Does Not Comply
Corrected Diskette Needed
never has*
*a response.
it is a
"header only."*

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/582,973

DATE: 06/26/2006
TIME: 13:30:45

Input Set : A:\sequence list.txt
Output Set: N:\CRF4\06262006\J582973.raw

139 Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met Asp His Thr Glu Ser Gly
140 210 215 220
141 Lys Ile Cys Gln Arg Trp Asp His Gln Thr Pro His Arg His Lys Phe
142 225 230 235 240
143 Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe Asp Asp Asn Tyr Cys Arg
144 245 250 255
145 Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys Tyr Thr Leu Asp Pro His
146 260 265 270
147 Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr Cys Ala Asp Asn Thr Met
148 275 280 285
149 Asn Asp Thr Asp Val Pro Leu Glu Thr Thr Glu Cys Ile Gln Gly Gln
150 290 295 300
151 Gly Glu Gly Tyr Arg Gly Thr Val Asn Thr Ile Trp Asn Gly Ile Pro
152 305 310 315 320
153 Cys Gln Arg Trp Asp Ser Gln Tyr Pro His Glu His Asp Met Thr Pro
154 325 330 335
155 Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu Asn Tyr Cys Arg Asn Pro
156 340 345 350
157 Asp Gly Ser Cys Ser Pro Trp Cys Phe Thr Thr Asp Pro Asn Ile Arg
158 355 360 365
159 Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys Asp Met Ser His Gly Gln
160 370 375 380
161 Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr Met Gly Asn Leu Ser Gln
162 385 390 395 400
163 Thr Arg Ser Gly Leu Thr Cys Ser Met Trp Asp Lys Asn Met Glu Asp5
164 405 410 415
165 Leu His Arg His Ile Phe Trp Glu Pro Asp Ala Ser Lys Leu Asn Glu
166 420 425 430
167 Asn Tyr Cys Arg Asn Pro Asp Asp Asp Ala His Gly Pro Trp Cys Tyr
168 435 440 445
169 Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr Cys Pro Ile Ser Arg Cys
170 450 455 460
171 Glu Gly Asp Thr Thr Pro Thr Ile Val Asn Leu Asp His Pro Val Ile
172 465 470 475 480
173 Ser Cys Ala Lys Thr Lys Gln Leu Arg Val Val Asn Gly Ile Pro Thr
174 485 490 495
175 Arg Thr Asn Ile Gly Trp Met Val Ser Leu Arg Tyr Arg Asn Lys His
176 500 505 510
177 Ile Cys Gly Gly Ser Leu Ile Lys Glu Ser Trp Val Leu Thr Ala Arg
178 515 520 525
179 Gln Cys Phe Pro Ser Arg Asp Leu Lys Asp Tyr Glu Ala Trp Leu Gly
180 530 535 540
181 Ile His Asp Val His Gly Arg Gly Asp Glu Lys Cys Lys Gln Val Leu
182 545 550 555 560
183 Asn Val Ser Gln Leu Val Tyr Gly Pro Glu Gly Ser Asp Leu Val Leu
184 565 570 575
185 Met Lys Leu Ala Arg Pro Ala Val Leu Asp Asp Phe Val Ser Thr Ile
186 580 585 590
187 Asp Leu Pro Asn Tyr Cys Thr Ile Pro Glu Lys Thr Ser Cys Ser

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/582,973

DATE: 06/26/2006
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Input Set : A:\sequence list.txt
Output Set: N:\CRF4\06262006\J582973.raw

188	595	600	605	
189	Val Tyr Gly Trp Gly Tyr Thr Gly Leu Ile Asn Tyr Asp Gly Leu Leu			
190	610	615	620	
191	Arg Val Ala His Leu Tyr Ile Met Gly Asn Glu Lys Cys Ser Gln His			
192	625	630	635	640
193	His Arg Gly Lys Val Thr Leu Asn Glu Ser Glu Ile Cys Ala Gly Ala			
194	645	650	655	
195	Glu Lys Ile Gly Ser Gly Pro Cys Glu Gly Asp Tyr Gly Gly Pro Leu			
196	660	665	670	
197	Val Cys Glu Gln His Lys Met Arg Met Val Leu Gly Val Ile Val Pro5			
198	675	680	685	
199	Gly Arg Gly Cys Ala Ile Pro Asn Arg Pro Gly Ile Phe Val Arg Val			
200	690	695	700	
201	Ala Tyr Tyr Ala Lys Trp Ile His Lys Ile Ile Leu Thr Tyr Lys Val			
202	705	710	715	720

723) delete - number the amino acids
under every 5.
amino acids

E--> 203 Pro Gln Ser
250 <210> SEQ ID NO: 4
251 <211> LENGTH: 39
252 <212> TYPE: DNA
253 <213> ORGANISM: Artificial Sequence

W--> 254 <220> FEATURE: 72207
254 <223> OTHER INFORMATION: (explain Artificial whenever 2217, 2227 or 2237 sequence is shown 39
255 <400> SEQUENCE: 4
256 tgcgtgaca atactatgca agacactgat gttcccttg
258 <210> SEQ ID NO: 5
259 <211> LENGTH: 41
260 <212> TYPE: DNA
261 <213> ORGANISM: Artificial Sequence

W--> 262 <220> FEATURE: 72207
262 <223> OTHER INFORMATION: (see item 11 on Error Summary Sheet)
263 <400> SEQUENCE: 5
264 ggcaaaaatt atatggcca gttatccaa acaagatctg g

41

266 <210> SEQ ID NO: 6
267 <211> LENGTH: 38
268 <212> TYPE: DNA
269 <213> ORGANISM: Artificial Sequence

W--> 270 <220> FEATURE: 72207
270 <223> OTHER INFORMATION: see item 11

271 <400> SEQUENCE: 6
272 tgcaaacagg ttctccaagt ttcccaagt gtatatgg
274 <210> SEQ ID NO: 7
275 <211> LENGTH: 38
276 <212> TYPE: DNA

38

277 <213> ORGANISM: Artificial Sequence
W--> 278 <220> FEATURE: 72207
278 <223> OTHER INFORMATION: (see item 11)
279 <400> SEQUENCE: 7
280 ggaaaggta ctctgcaaga gtctgaaata tgtgctgg

38

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/582,973

DATE: 06/26/2006
TIME: 13:30:45

Input Set : A:\sequence list.txt
Output Set: N:\CRF4\06262006\J582973.raw

283 <211> LENGTH: 38
284 <212> TYPE: DNA
285 <213> ORGANISM: Artificial Sequence
W--> 286 <220> FEATURE: *insert 12207*
286 <223> OTHER INFORMATION: *see item 11*
OKC 287 <400> SEQUENCE: 8
288 ggtgatacca cacctggaat agtcaattta gaccatcc

38

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5

<210> 1
<211> 728
<212> PRT
<213> Homo Sapiens
<220> Hepatocyte growth factor move to <223> line
<223> 6
<400> 1

10/582,973 6

<210> 3
<211> 2172 Sapiens
<212> DNA
<213> Homo sapience *move to C2237 line*
<220> Hepatocyte growth factor of five amino acids-deleted type
<223> 3
<400> 3

VERIFICATION SUMMARY DATE: 06/26/2006
PATENT APPLICATION: US/10/582,973 TIME: 13:30:46

Input Set : A:\sequence list.txt
Output Set: N:\CRF4\06262006\J582973.raw

L:3 M:283 W: Missing Blank Line separator, <120> field identifier
L:4 M:283 W: Missing Blank Line separator, <130> field identifier
L:5 M:270 C: Current Application Number differs, Replaced Current Application No
L:5 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:5 M:283 W: Missing Blank Line separator, <160> field identifier
L:6 M:283 W: Missing Blank Line separator, <210> field identifier
L:10 M:283 W: Missing Blank Line separator, <220> field identifier
L:10 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:12 M:283 W: Missing Blank Line separator, <400> field identifier
L:12 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:11
L:110 M:283 W: Missing Blank Line separator, <220> field identifier
L:110 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:112 M:283 W: Missing Blank Line separator, <400> field identifier
L:112 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:111
L:203 M:252 E: No. of Seq. differs, <211> LENGTH:Input:723 Found:688 SEQ:2
L:209 M:283 W: Missing Blank Line separator, <220> field identifier
L:209 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:211 M:283 W: Missing Blank Line separator, <400> field identifier
L:211 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:210
L:254 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:255 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:4
L:255 M:283 W: Missing Blank Line separator, <400> field identifier
L:255 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:254
L:262 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:263 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:5
L:263 M:283 W: Missing Blank Line separator, <400> field identifier
L:263 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:262
L:270 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:271 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:6
L:271 M:283 W: Missing Blank Line separator, <400> field identifier
L:271 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:270
L:278 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:279 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:7
L:279 M:283 W: Missing Blank Line separator, <400> field identifier
L:279 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:278
L:286 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:287 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:8
L:287 M:283 W: Missing Blank Line separator, <400> field identifier
L:287 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:286